AMENDMENTS TO THE CLAIMS

1. (Withdrawn) A compound, comprising a) a first amino acid sequence comprising at least a portion of a histone amino terminal tail, said first amino acid sequence linked to b) a second amino acid sequence comprising at least a portion of a histone acetyltransferase.

2. (Withdrawn) The compound of Claim 1, wherein said second amino acid sequence comprises the active catalytic domain of Gcn5.

3. (Withdrawn) The compound of Claim 1, wherein said second amino acid sequence comprises a catalytically inactive portion of Gcn5.

4. (Withdrawn) The compound of Claim 1, wherein said first amino acid sequence comprises the histone H3 tail.

5. (Withdrawn) The compound of Claim 1, wherein said first amino acid sequence comprises the histone H4 tail.

6. (Withdrawn) The compound of Claim 1, wherein said compound comprises a fusion protein.

7. (Withdrawn) The compound of Claim 1, wherein said compound exhibits autoacetylation.

8. (Withdrawn) The compound of Claim 1, further comprising a DNA binding moiety.

9. (Withdrawn) The compound of Claim 6, wherein said DNA binding moiety is linked to said first amino acid sequence.

10. (Withdrawn) The compound of Claim 8, wherein said DNA binding moiety comprises the Gal4 DNA binding domain.

11. (Withdrawn) The compound of Claim 9, further comprising a detectable moiety linked to said second amino acid sequence.

12. (Withdrawn) The compound of Claim 11, wherein said detectable moiety comprises an epitope.

13. (Withdrawn) The nucleic acid encoding the fusion protein of Claim 11.

14. (Withdrawn) An expression vector comprising the nucleic acid of Claim 13.

15. (Withdrawn) Yeast transformed with the expression vector of Claim 14.

16. (Withdrawn) A whole cell extract of the yeast of Claim 15.

17. (Currently amended) A method for detecting protein-protein interactions, said interactions requiring a post translational modification of one of the said proteins, said method comprising: (a) providing a host cell comprising a detectable gene wherein the detectable gene expresses a detectable protein when the detectable gene is activated by an amino acid sequence comprising ~~including~~ a transcriptional activation domain when the transcriptional activation domain is in sufficient proximity to the detectable gene; (b) providing a first chimeric gene that is capable of being expressed in the host cell, the first chimeric gene comprising a DNA sequence that encodes a first hybrid protein, the first hybrid protein comprising: (i) a DNA-binding moiety that recognizes a binding site on the detectable gene in the host cell, said DNA-binding moiety comprising the Gal4 DNA binding domain, hereinafter GDBD; (ii) a first test protein or fragment thereof, comprising a reactive moiety capable of being modified through catalysis, that is to be tested for interaction with at least one second test protein or fragment thereof, said reactive moiety comprising a histone amino terminal tail capable of being acetylated by Gcn5; and (iii) a catalytic moiety that is capable of catalyzing said first test protein, said catalytic moiety comprising the catalytic domain of Gcn5; (c) providing a second chimeric gene that is capable of

being expressed in the host cell, the second chimeric gene comprising a DNA sequence that encodes a second hybrid protein, the second hybrid protein comprising: (i) the transcriptional activation domain; and (ii) a second test protein or fragment thereof that is to be tested for interaction with the first test protein or fragment thereof when said first test protein has been modified by the catalysis of said reactive moiety to create a modified first test protein; wherein interaction between the first modified test protein and the second test protein in the host cell causes the transcriptional activation domain to activate transcription of the detectable gene; (d) introducing the first chimeric gene and the second chimeric gene into the host cell; (e) subjecting the host cell to conditions under which the first hybrid protein and the second hybrid protein are expressed in sufficient quantity for the detectable gene to be activated; and (f) determining whether the detectable gene has been expressed to a degree greater than expression in the absence of an interaction between the first test protein and the second test protein.

18. (Canceled)

19. (Currently amended) The method of Claim 17, wherein said first test protein and said second test protein are encoded on a library of plasmids containing DNA inserts~~, derived~~ selected from the group consisting of genomic DNA, cDNA, and synthetically generated DNA.

20. (Currently amended) The method of claim 17, wherein said first test protein ~~are derived are derived~~ is selected from the group consisting of bacterial protein, viral protein, oncogene-encoded protein, fungal protein and plant protein.

21. (Withdrawn) A compound, comprising a) a first amino acid sequence comprising at least a portion of an enzyme substrate, said first amino acid sequence linked to b) a second amino acid sequence comprising at least a portion of an enzyme capable of enzymatically converting said first amino acid sequence.

22. (Withdrawn) A nucleotide sequence selected from a group consisting of SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 29, 31, 33, 35 and 37.

23. (Withdrawn) An amino acid sequence selected form a group consisting of SEQ ID NOS: 15, 16, 17, 18, 19, 20 21, 22, 23, 24 , 25, 26, 27, 28, 30, 32, 34, 36 and 38.

24. (Currently amended) A method for detecting protein-protein interactions, comprising: (a) providing a host cell comprising a detectable gene, wherein the detectable gene expresses a detectable protein when the detectable gene is activated by an amino acid sequence comprising a transcriptional activation domain; (b) providing a first chimeric gene that is capable of being expressed in said host cell, the first chimeric gene comprising a DNA sequence that encodes a first hybrid protein, the first hybrid protein comprising: (i) a DNA-binding moiety that recognizes a binding site on the detectable gene in the host cell, said DNA-binding moiety comprising the Gal4 DNA binding domain, hereinafter GDBD; (ii) a reactive moiety capable of being modified through catalysis, said reactive moiety comprising a histone amino terminal tail capable of being acetylated by Gcn5; and (iii) a catalytic moiety that is capable of catalyzing said reactive moiety, said catalytic moiety comprising the catalytic domain of Gcn5 ; (c) providing a second chimeric gene that is capable of being expressed in the host cell, the second chimeric gene comprising a DNA sequence that encodes a second hybrid protein, the second hybrid protein comprising a transcriptional activation domain; and (d) introducing the first chimeric gene and the second chimeric gene into the host cell under conditions wherein the first hybrid protein and the second hybrid protein are expressed.

25. (Original) The method of claim 24, comprising determining whether the detectable gene has been expressed.

26. (Withdrawn) A compound, comprising a) a first amino acid sequence comprising at least a portion of a histone amino terminal tail, said first amino acid sequence linked to b) a second amino acid sequence comprising at least a portion of a protein kinase.

27. (Withdrawn) The compound of Claim 26, wherein said second amino acid sequence comprises the active domain of IPL1 kinase.

28. (Withdrawn) A compound, comprising a) a first amino acid sequence comprising at least a portion of a carboxy terminal domain, said first amino acid sequence linked to b) a second amino acid sequence comprising at least a portion of protein kinase.

29. (Withdrawn) The compound of Claim 28, wherein said second amino acid sequence comprises the active domain of KIN28 kinase.